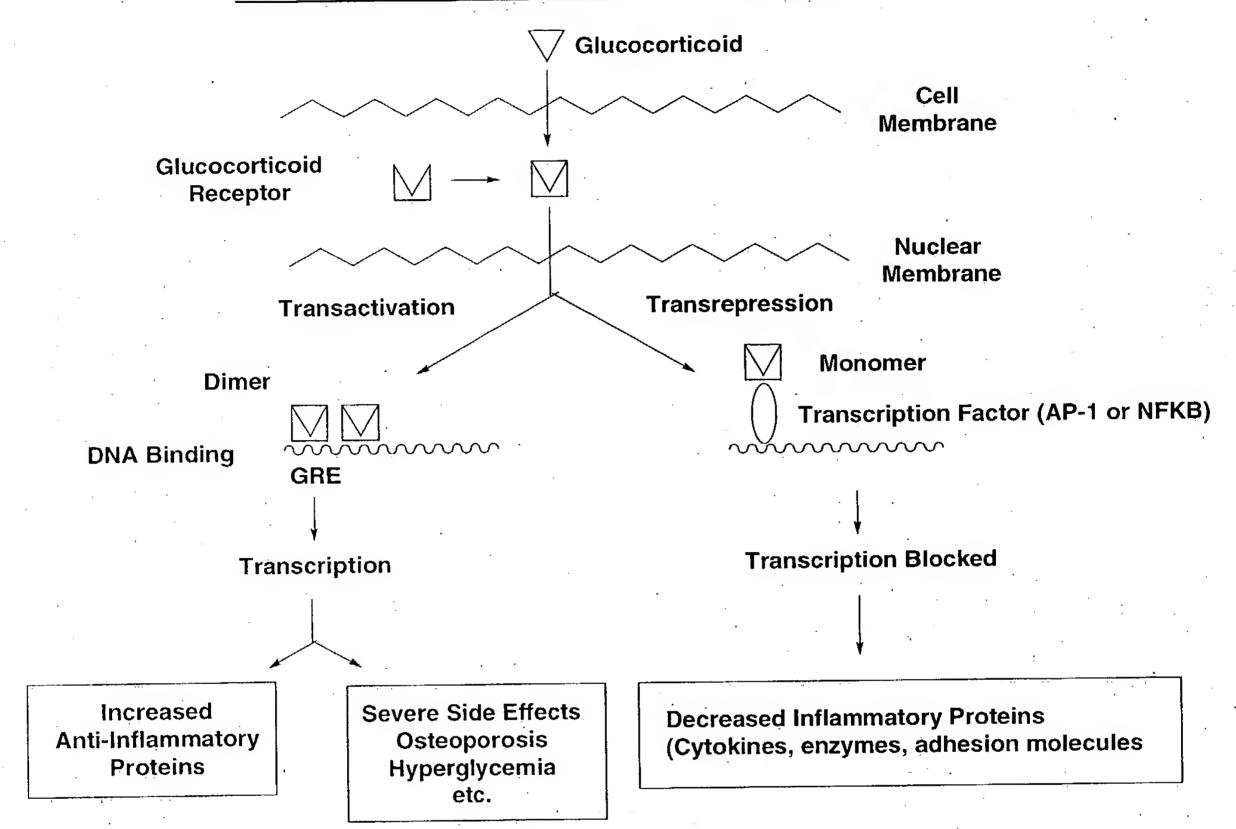
**FIGURE 1** 

## Dissociated Steroid: Transrepression > Transactivation



#### FIGURE 2

			•					
RXRalpha	225	S	ANEDM			PVE.RILEAE	LAVE PKTET	•
-					•			
RARgamma	182	Ъ	SPQ. LEE		• • • • • • • • •	LIT.KVSKAH	QEIF.P	
PR	682		0 .	LI.	P	PLINLLMSIE	PD.V	
		,					0.00 (00)	•
AR	669					IFLNVLEAIE	1	
ERalpha	305				.SLALSLTAD	QMVSALLDAE	PPI	
ERbeta	261					QLVLTLLEAE		
•						*C.U***********************************		
VitDR	120	.LRPKL	SEEQQR		• • • • • • • • •	IIA.ILLDAH	HKTY.D	
PPARgamma	207	E	SAD. LRA			LAK.HLYDSY	IKSF.P	·
						\$2000000 \$210000000000000000000000000000	00000000000000000000000000000000000000	•
MR	731					SPVMVLENIE	1 (4) 1 (4) 10 10 10 10 10 10 10 10 10 10 10 10 10	
TRbeta	211	KPEP	TDE . EWE			LIK.TVTEAH	VATNAQ	
GR	523					TLVSLLEVIE		
GIX	223	• • • • • • • • • • •					**************************************	•
RXRalpha	249	YVEANMGLNP	SSPNDPVTN.		IC.			
***								
RARgamma	203	•				LCQL.GKYTT		• •
PR	699		I	YAGHDNTKPD	TSSSLLTS			
AR	685		V	CAGHDNNOPD	SEAALLSS.			
Α						•		•
ERalpha	327		· · · · · · · · · · · · · · · · · · ·	YSEYDPTRPF	SEASMMGL		• • • • • • • • • •	
ERbeta	281		V	LISR	TEASMMMS.			
• •	•		•			·		
VitDR	145					•••••		
PPARgamma				·			·	
			•		· ·			
	750				,			
TRbeta	236			· · · · · · · · · · · · · · · · · · ·		SHWKQKRKFL	P	
GR.	544		· T.	VAGVDSSVPD	STWRIMTT			•
GIC .	944	• • • • • • • • •						,
			,		-			•
RXRalpha								
	211					•		
RARgamma	214				·			' '
PR								
AR .				·				
		·						
ERalpha								•
ERbeta								
•	1					•		
VitDR	155				·			
PPARgamma	228			LTKAKAR	ALLTGKTTDK	SPFVIYDMNS	LMMGEDKIKF	, •
-								
MR						,	•	•
ŢRbeta	248	EDIGQAPK	V					•
GR								•
			• • • • • • • • • •					•
			•	20,440,40000				
RXRalpha	271						9000006	• *
_	223			OAADK	OLFTLVEWAK	RIPHFSELPL	DDOVILLRAG	- · ·
RARgamma	2.2.3			200000 20000		RIPHFSELPL	220,744	• · ·
PR ·	220		DLGLWDK	FSELATK	CIIKIVEFAK	RLPGFTGLSI	ADQITLLKAA	
L IV	718		DLGLWDK	FSELATK	CIIKIVEFAK		ADQITLLKAA	
	718		DLGLWDK	FSELATK	CIIKIVEFAK QLLSVVKWSK	RLPGFTGLSI SLPGFRNLHI	ADQITLLKAA DDQITLIQYS	
AR	718 705		DLGLWDK	FSELATKLNQLGERLNELGER	CIIKIVEFAK QLLSVVKWSK QLVHVVKWAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV	ADQITLLKAA DDQITLIQYS DDQMAVIQYS	
	718		DLGLWDK	FSELATKLNQLGERLNELGERLTNLADR	CIIKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA	
AR ERalpha	718 705		DLGLWDK	FSELATKLNQLGERLNELGERLTNLADR	CIIKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA	
AR ERalpha ERbeta	718 705 345 294		DLGLWDK	FSELATKLNQLGERLNELGERLTNLADRLTKLADK	CIIKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC	
AR ERalpha ERbeta VitDR	718 705 345 294 172		DLGLWDK	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS	
AR ERalpha ERbeta	718 705 345 294 172		DLGLWDK	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS	
AR ERalpha ERbeta VitDR PPARgamma	718 705 345 294 172 265	KHITPLQEQS	DLGLWDK	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVE	CIIKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG	
AR ERalpha ERbeta VitDR PPARgamma MR	718 705 345 294 172 265 769	KHITPLQEQS	DLGLWDK	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK	CIIKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS	
AR ERalpha ERbeta VitDR PPARgamma	718 705 345 294 172 265	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR	718 705 345 294 172 265 769	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	
AR ERalpha ERbeta VitDR PPARgamma MR TRbeta	718 705 345 294 172 265 769 257	KHITPLQEQS	DLGLWDKOLGLWDKQLSMLPH KEVAIRIFQGDLEAFSH	FSELATKLNQLGERLNELGERLTNLADRLTKLADK LADLVSY CQFRSVELNRLAGK FTKIITP	CITKIVEFAK QLLSVVKWSK QLVHVVKWAK ELVHMINWAK ELVHMISWAK SIQKVIGFAK AVQEITEYAK QMIQVVKWAK AITRVVDFAK	RLPGFTGLSI SLPGFRNLHI ALPGFRNLHV RVPGFVDLTL KIPGFVELSL MIPGFRDLTS SIPGFVNLDL VLPGFKNLPL KLPMFCELPC	ADQITLLKAA DDQITLIQYS DDQMAVIQYS HDQVHLLECA FDQVRLLESC EDQIVLLKSS NDQVTLLKYG EDQITLIQYS EDQIILLKGC	

## FIGURE 2 (continued)

· *	RXRalpha	306	WNELLIASFS	HRSIAV	KDGILLAT	GLHVHRN	SAHSAG	VG	
	RARgamma	267	The state of the s		000	GLTLNRT			
	PR	755			22,000	DLILNEQ			
				**************************************	\$200		·		•
	AR	742	* County of the		27%	DLVFNEY	• •		•
	ERalpha	382	WLEILMIGLV		27722			MV	
	ERbeta	331	WMEVLMMGLM	WRSID	.HPGKLIFAP	DLVLDRD	E.GKCVEG	IL	
•	VitDR	216	AIEVIMLRSN	ESFTMD.	DMSWTCG	N.QDYKYRVS	DVT	KAGH	
	PPARgamma	322	VHEIIYTMLA	SLMNK	DGVLISE	GQGFMTR	E.FLK	SLRK	
	MR	806	WMCLSSFALS	WRSYKH	TNSOFLYFAP	DLVFNEE	.KMHOSAM	YE	
	TRbeta	301	CMEIMSLRAA	The state of the s	4.0 6.0	EMAVTRG	* .:		
. 1	GR	600				DLIINEQ	·	•	
•.	·	000	W111 E11171/1710	VII.D 1111.	DOMINDUCT ALL	DDTINDQ	·······································		
	,	2.45	, TH DD	**************************************	DMOMBURDE		DD GWG I G		
•	RXRalpha		A.IF.DR			3000		,	•
	<b>-</b>	305	·			LLSAICL.IC	·		
	PR	796	S.LC.LT	MWQIPQEFV.	KLQVSQEEFL	CMKVLLL.LN	.TIP.LEGLR		
·	AR	783	S.QC.VR	MRHLSQEFG.	WLQITPQEFL	CMKALLL.FS	.IIP.VDGLK		
·	ERalpha	422	E.IF.DM	LLATSSRFR.	MMNLQGEEFV	CLKSIILLNS	.GV	YTF.LSSTLK	•
	ERbeta	371	E.IF.DM	LLATTSRFR.	ELKLOHKEYL	CVKAMILLNS		LVTAT.Q	
· / /	VitDR	255		LIKFOVGLK.	* *************************************	LLMAICI.VS		·	
	PPARgamma		PFGD.FM.EP	~	23.099	67972			
•	MR		LC.QG	,	27827 107 T	¥39		·	•
					- CO	1.000			•
	TRbeta	339	•		- 700000				• 1
	GR ·	641	DQCKH	MLYVSSELH.	RLQVSYEEYL	CMKTLLL.LS	.SVP.KDGLK	•••••	
					•			·	
	RXRalpha	386	NPAEVEA	LREKVYASLE	AYCKHKYP	EQPG	RFAKLLL	RLPALRSIGL	* :
	RARgamma	336	EPEKVDK	LQEPLLEALR	LYARRRRP	SQPY	MFPRMLM	KITDLRGIST	· .
· _	PR.	837	SOTOFEE	MRSSYIRELI	KAIGLRO	KGVVS	SSORFYOLTK	LLDNLHDLVK	
		824						LLDSVQPIAR	
	ERalpha	467				LTLQQ	-		; · i.
	· -			4			-		
	ERbeta	411	-			ISSQQ		·	an 3
•		297				PP.L	_		
	PPARgamma	402	:NVKPIED	IQDNLLQALE	LQLKLNHP	ESSQ	LFAKLLQ	KMTDLRQIVT	
	MR	888	SQAAFEE	MRTNYIKELR	KMVT.KCPNN	SQ	SWQRFYQLTK	LLDSMHDLVS	•
	TRbeta	3,80	CVERIEK	YQDSFLLAFE	HYINYRKH	HVTH	FWPKLLM	KVTDLRMIGA	
	GR	681	SQELFDE	IRMTYIKELG	KAIVKRE	GNSSQ	NWQRFYQLTK	LLDSMHEVVE	
			•		•				
	RXRalpha	432	KCLEHLFFFK	LIGDTPIDTF	LMEMLEAPHO	MT			
	RARgamma	382	· · · · · · · · · · · · · · · · · · ·		_	ITLKMEI			·
		886							
	PR								
	AR	873	•			• • • • • • • • • • • • • • • • • • • •			
	ERalpha	519				• • • • • • • • • • • • • • • • • • • •			
	ERbeta	463				•		L	
	VitDR	342				RCLSFQP			
	PPARgamma	448	EHVQLL			QVIKKTET	DMSLHP	LLQEIYKDL.	
	MR	937	•				-		
	TRbeta	426				LHMKVEC			
	GR	730							
		•							
•									
								•	
-					-		•		·
								•	9
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								•	

### FIGURE 2 (continued)

RXRalpha RARgamma PR AR ERalpha ERbeta VitDR PPARgamma MR TRbeta GR	893 880 526 470 944 737	.NTFIQSRAL .DLLIKSHMV .SMKCKNV. NMKC	SVEFPEMMSE SVDFPEMMAE	VIAAQLPKIL IISVQVPKIL	AGMVKPLLFH SGKVKPIYFH SGKVKPIYFH SGNAKPLYFH	K	ML
RXRalpha RARgamma PR AR ERalpha ERbeta VitDR PPARgamma MR TRbeta GR	482 477 984 453	LLLEMLNAHV	LRYK.				

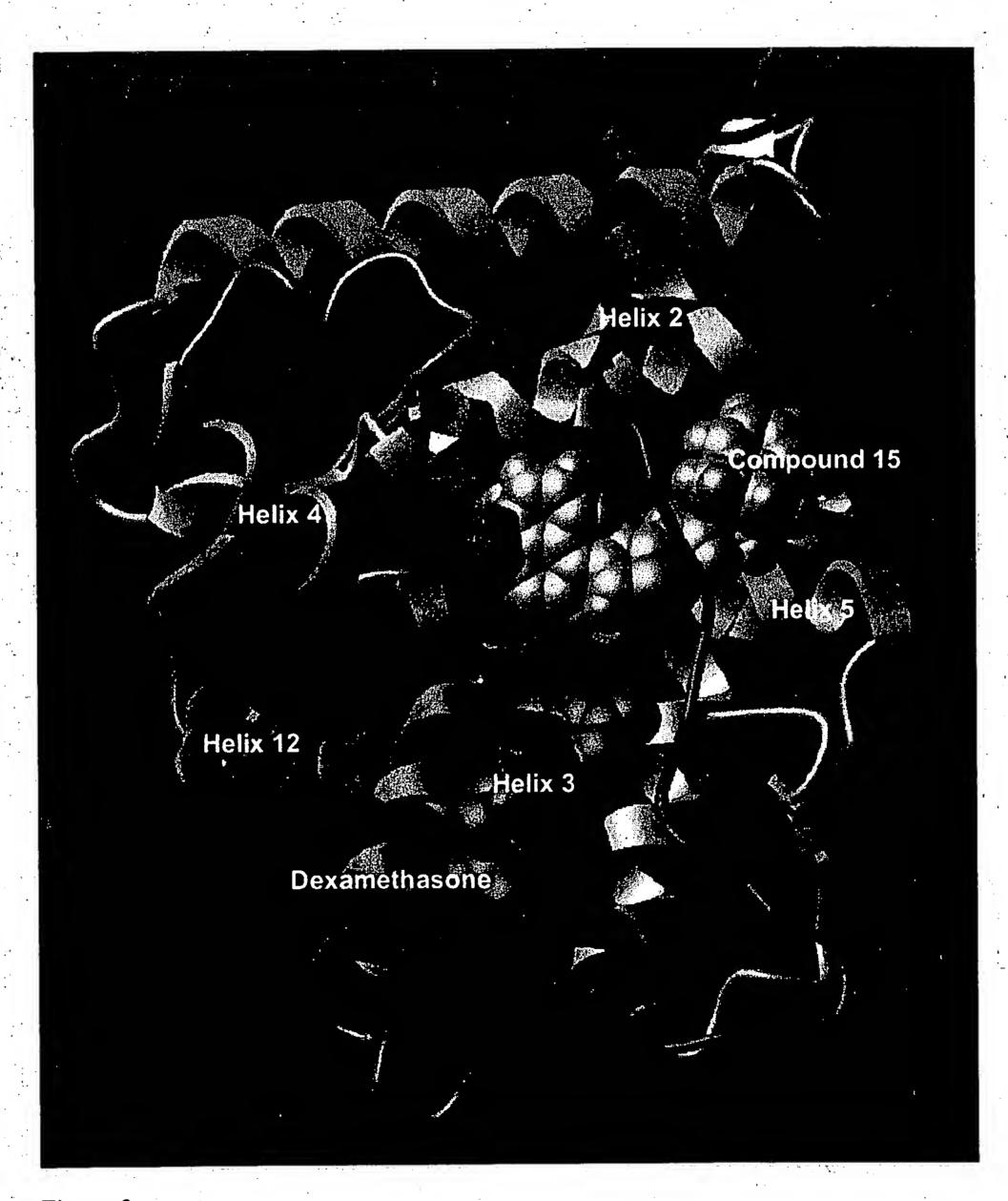
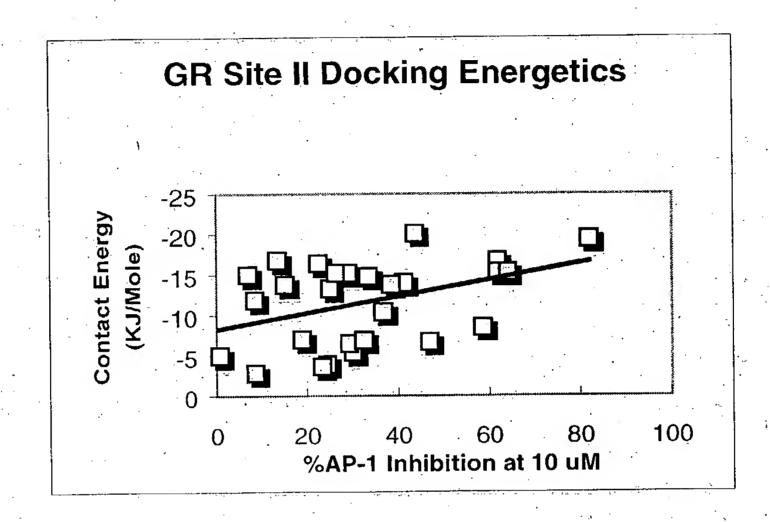


Figure 3.



#### FIGURE 6

								• • • •
• .	u87951 Squirrel	•	MDSKESLTP.	GKEENPSSVL	TQERGNVMDF	CKILRGGATL	KVSVSSTSLA	•
	AF141371 Pig							•
	113196 Guinea Pig	÷.	MDLKESVTSS	KEVPSSVI	GSERRNVTDF	YKTVRGGATV	KVSASSPSLA	•
	u87953 Marmoset		• • •	-	TQERGNVMDF			
	•				,			•
	u87952 Ma'z Monkey				TOERGNVMDF	•		
	Human			• •	AQERGDVMDF			
	m14053 rat		MDSKESLAPP	ĢRDEVPGSLL	GQGRGSVMDF	YKSLRGGATV	KVSASSPSVA	
	x04435 mouse		MDSKESLAPP	GRDEVPSSLL	GRGRGSVMDL	YKTLRGGATV	KVSASSPSVA	
		•	•					
					. ;			
	u87951 Squirrel	•	AASOSDSKOO	RLLVDFPKGS	VSNAQQ		PDLS	
	AF141371 Pig				AVSQPDSKQQ		•	
				, .			· ·	Te e
	113196 Guinea Pig				GSNAQQ	•		•
•	u87953 Marmoset			_	VSNAQQ		•	•
	u87952 Ma'z Monkey						PDLS	
	Human		VASQSDSKQR	RLLVDFPKGS	VSNAQQ		PDLS	
	m14053 rat - `		AASQADSKQQ	RILLDFSKGS	TSNVQQRQQQ	QQQQQQQQQQ	QQQQQQPGLS	
	x04435 mouse						QQQQPQPDLS	
					<del></del>	1		
				•				•
			WATTER CMCT V	мертртити	NDLGFPQQGQ	TOTOCOUPING	OLL PPCTAMI	
•	u87951 Squirrel	•			· .	**	•	
	AF141371 Pig		•		SDLGFPQQGQ			
	113196 Guinea Pig						RLLEESIANL	
	u87953 Marmoset	· ·	KAVSLSMGLY	MGETETKVMG	NDLGFPQQGQ	ISLSSGETDL	QLLEESIANL	· 
	u87952 Ma'z Monkey		KAVSLSMGLY	MGETETKVMG	NDLGFPQQGQ	ISLSSGETDĻ	QLLEESIANL	•
* *	Human		KAVSLSMGLY	MGETETKVMG	NDLGFPQQGO	ISLSSGETDL	KLLEESIANL	
	m14053 rat				NDLGYPQQGQ	•		
	x04435 mouse				NDLGYPQQGQ	•		
	Yourship mode		TOTA DIPORTOR T	LICELLITICATIO	HEHOTT AKOK		المفاق المنظم المناسبة	
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	07051 ~ ' ' '	•	in amarines	Voga godina	3 j <u>arrananaa.</u>	1105110050	r ważma artas	
٠ ,	u87951 Squirrel			·			LKGQTGSNGG	
	AF141371 Pig				APAEKAFPKŢ			
	113196 Guinea Pig		·	,			LKSQAGTNGG	
	u87953 Marmoset		NRSTSVPENP	KSSASSSVSA	APKEKEFPKT	HSDVSSEQQN	LKGQTGTNGG	
	u87952 Ma'z Monkey		NRSTSVPENP	KSSASSSVSA	APKEKEFPKT	HSDVSSEQQN	LKGQTGTNGG	
	Human						LKGQTGTNGG	•
	m14053 rat				•		RKSQTGTNGG	
	x04435 mouse						RKSQPGTNGG	-
	<b>ずらきょうつ HOORSE</b>		MINDIDIKETINE	MODIIMACH	TITUKELEQI	τιοητ <sub>ι</sub> όομδδιν	тию Хів атмаа	•
	•					•.		
	u87951 Squirrel				•	,	DLLIDENCLL	• '
	AF141371 Pig		NVKLFTTDQS	TFDIWRKKLQ	DLELPSGSPG	KEŢŞĘSPWŞŞ	DLLIDENCLL	
	113196 Guinea Pig		NVK.FPPDQS	TFDILK	DLEFSSGSPG	KERSESPWRP	DLLMDESCLL	
	u87953 Marmoset		NAKLCTADOS	TFDILO	DLEFSSGSPG	KETNQSPWRS	DLLIDENCLL	
	u87952 Ma'z Monkey		•	· -			DLLIDENCLL	
	Human				•		DLLIDENCLL	
	·				DLEFSAGSPS			
	m14053 rat			· ·		•		
	x04435 mouse		PAVTILIDÕŽ	renrpŐ	DLEFSAGSPG	VEINESEMKS	קק י אמעדיייים	
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4								

## FIGURE 6 (Continued)

-	u87951 Squirrel		SPLAGEEDSF	LLEGNSNEDC	KPLILPDTKP	KIKDNGDLVL	SSSSNVTLPQ	
	AF141371 Pig		SPLAGEEDPF	LLEGSSTEDC	KPLVLPDTKP	KVKDNGELIL	PSPNSVPLPQ	
	113196 Guinea Pig		SPLAGEDDPF	LLEGNSNEDC	KPLILPDTKP	KIKDNGDGIL	SSSNSVPQPQ	
	u87953 Marmoset		SPLAGEEDSF	LLEGNSNEDC	KPLILPDTKP	KIKDNGDLVL	SSSSNVTLPQ	
	u87952 Ma'z Monkey		SPLAGEEDSF	LLEGNSNEDC	KPLILPDTKP	KIKDNGDLVL	SSSSNVTLPQ	
	Human		SPLAGEDDSF	LLEGNSNEDC	KPLILPDTKP	KIKDNGDLVL	SSPSNVTLPQ	
	m14053 rat		SPLAGEDDPF		KPLILPDTKP	•	SSPSSVALPQ	
	$\times 04435$ mouse		SPLAGEDDPF		KPLILPDTKP		SSPSSVALPQ	
	Notato monac	*					₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩	•
			•			•	•	
•	u87951 Squirrel	· · · · ·	VKTEKEDETE	LCTPGVIKQE	KLSTVYCOAS	FPGANTIGNK	MSATSTHGVS	
	AF141371 Pig		VKTEKEDFIE		KLGPAYCQAS			
	113196 Guinea Pig	. ·	VKIGKEDFIE	•	KLGPVYCQAS	·		
			VKTEKEDFIE	•	KLSTVYCQAS		•	
	u87953 Marmoset	- "	VKTEKEDFIE		KLSTVYCQAS	•	·	
	u87952 Ma'z Monkey				KLGTVYCQAS			
	Human		VKTEKEDF1E		7			
	m14053 rat							
	x04435 mouse	,	AK.LEKDDE TË	LCTPGVIKQE	KLGPVICQAS	FSGINITIGNK	MSAISVAGVS	
	00054: 0 1		magaaa <b>M</b>	MNIMA CECOO	ODOKOTEMIA		NIDGOCCCODDNI	
	u87951 Squirrel							
	AF141371 Pig			MNTAASLSKQ				
	113196 Guinea Pig	٠.		MNTA.SLSQQ		• •		
	u87953 Marmoset		TSGGQMYHYD		QDQKPIFNVI			
	u87952 Ma'z Monkey		TSGGQMYHYD	_		PPIPVGSENW	NRCQGSGDDN	
	Human	•	TSGGQMYHYD	MNTA.SLSQQ		PPIPVGSENW	NRCQGSGDDN	
	m14053 rat		TSGGQMYHYD		QDQKPVFNVI		NRCQGSGEDS	
	x04435 mouse		TSGGQMYHYD	MNTA.SLSQQ	QDQKPVFNV1	PPIPVGSENW	NRCQGSGEDN	
				•		•		
			•	· .		•		
•	u87951 Squirrel	:	LTSLGTLNFP	GRTVFSNGYS	SPSMRPDVSS	PPSSSSTATT	GPPPKLCLVC	
	AF141371 Pig		LTSLGTLNFS	GRSVFSNGYS	SPGMRPDVSS	PPSSSSAAT.	GPPPKLCLVC	•
	113196 Guinea Pig		LTSLGTVNFP	GRSVFSNGYS	SPGLRPDVSS	PPSSSST.TT	GPPPKLCLVC	
	u87953 Marmoset		LTSLGTLNFP	GRTVFSNGYS	SPSMRPDVSS		GPPPKLCLVC	
	u87952 Ma'z Monkey		LTSLGTLNFP	GRTVFSNGYS	SPSMRPDVSS	PPSSSSTATT	GPPPKLCLVC	
	Human		LTSLGTLNFP	GRTVFSNGYS	SPSMRPDVSS	PPSSSSTATT	GPPPKLCLVC	
	m14053 rat	:	LTSLGALNFP	GRSVFSNGYS	SPGMRPDVSS	PPSSSSAAT.	GPPPKLCLVC	
	x04435 mouse		LTSLGAMNFA	GRSVFSNGYS	SPGMRPDVSS	PPSSSSTAT.	GPPPKLCLVC	
	-			•		•		
			• -			· -		
	u87951 Squirrel		SDEASGCHYG	VLTCGSCKVF	FKRAVEGQHN	YLCAGRNDCI	IDKIRRKNCP	
	AF141371 Pig		SDEASGCHYG		FKRAVEGQHN		IDKIRRKNCP	
	113196 Guinea Pig			VLTCGSCKVF			IDKIRRENCP	
	u87953 Marmoset			VLTCGSCKVF	•	• •		
	u87952 Ma'z Monkey			VLTCGSCKVF		• •		
	Human			VLTCGSCKVF			•	
	m14053 rat			VLTCGSCKVF		.*		
	x04435 mouse			VLTCGSCKVF			·	
	110 4 4 9 0 1110 419 0		,		~ # - 1 mi A' X' + + 1 A		and the second s	
			-					

# FIGURE 6 (Continued)

	,						•		
	u87951	Squirrel		ACRYRKCLQA	GMNLEARKTK	KKIKGIQQAT	TGVSQETSEN	PANKTIVPAT	
	AF14137	•				KKIKGIQQAT	•	SANKTIVPAT	
		Guinea Pig		ACRYRKCLQA		KKIKGIQQAT		P.NKTIVPAT	,
		Marmoset		ACRYRKCLQA		KKIKGIQQAT		PANKTIVPAT	
		Ma'z Monkey		ACRYRKCLQA		KKIKGIQQAT	•	PANKTIVPAT	
	Human					KKIKGIQQAT		PGNKTIVPAT	
	m14053	rat				KKIKGIQQAT		P.NKTIVPAA	
	$\times 04435$	•		•	•	KKIKGIQQAT		.ANKTIVPAA	
	Yorkan 5	Ino Quo C		1101/11/11/04/21			110 (15 22 15 24)		
				•	• • •				
	u87951	Squirrel	525	LPOLTPTLVS	LLEVIEPEVL	YAGYDSTVPD	STWRIMTTLN	MLGGRQVIAA	
	AF14137	<del>-</del>			LLEVIEPEVL		STWRIMTALN	MLGGROVIAA	
		Guinea Pig	•		LLEVIEPEVI		STWRIMTTLN	MLGGRQVIAA	•
		Marmoset		LPQLTPTLVS	***************************************	YAGYDSTVPD	STWRIMTTLN	MLGGRQVIAA	
		Ma'z Monkey	525		LLEVIEPEVL	YAGYDSTVPD	STWRIMTTLN	MLGGRQVIAA	
٠, ،	Human		525		LLEVIEPEVL	YAGYDSSVPD	STWRIMTTLN	MLGGRQVIAA	
	m14053	rat		LPQLTPTLVS	C. C	YAGYDSSVPD	SAWRIMTTLN	MLGGRQVIAA '	•
	x04435		. ,		LLEVIEPEVL	·	SAWRIMTTLN	MLGGRQVIAA	
	NO 4 122		, ,	# 2 - + 1 - 1 - 1					
						•		•	
	u87951	Squirrel	575	VKWAKAIPGF	RNLHLDDQMT	LLQYSWMFLM	AFALGWRSYR	QASSNLLCFA	
	AF14137					LLQYSWMFLM		N. Maria Ladi M. Santania	
		Guinea Pig	569	and and		LLQYSWMFLM		3,000 100 000 000 6,00 m (4,000)	
	•	Marmoset	575	Commence		LLQYSWMFLM		6/00000	
		Ma'z Monkey	575	VKWAKAIPGF		LLQYSWMFLM		1000000	
	Human		575	4.00 C 3.00 C 3.		LLQYSWMFLM		7000 A	
,	m14053	rat	593	6 17% (10.00 17%) (10.00 17%) 8 17% (10.00 17%) (10.00 17%)		LLQYSWMFLM		585,000	
	x04435	, ,	581	27-1-10-10-10-10-10-10-10-10-10-10-10-10-1		LLQYSWMFLM	2000-201 <b>2                                   </b>	19:00	
				entropy and congress			narmen, m. m. negati eta (h. 1		
						•			
٠.	u87951	Squirrel	625	PDLIINEQRM	TLPCMYDQCK	HMLYVSSELH	RLQVSYEEYL	CMKTLLLLSS	
	AF14137		589	PDLVÍNEQRM	ALPCMYDQCR	HMLYVSSELQ	RLQVSYEEYL	CMKTLLLLSS	
		Guinea Pig		2000		YMLYVSSELK	-than 20000 S	CMKTLLLLSS	
		Marmoset		80.00		HMLYVSSELH		CMKTLLLLSS	
		Ma'z Monkey		22003		HMLYVSSELH	. 10000000000	CMKTLLLLSS	
	Human	· · · · · · · · · · · · · · · · · · ·		9004		HMLYVSSELH		CMKTLLLLSS	
	m14053	rat	•	\$0.000 \$0.000		HMLFVSSELQ	. 300000	CMKTLLLLSS	
	$\times 04435$	,		800%		HMLFISTELQ	71507030400	200	
	,			3945			110 110 110 110 110 110 110 110 110 110	***************************************	
	•				•			•	
	u87951	Squirrel		VPKDGLKSQE	LFDEIRMTYI	KELGKAIVKR	EGNSSQNWQR	FYQLTKLLDS	
	AF14137	1 Pig		VPKDGLKSQE	LFDEIRMTYI	KELGKAIVKR	EGNSSQNWQR	FYQLTKLLDS	
	113196	Guinea Pig		VPKEGLKSQE	LFDEIRMTYI	KELGKAIVKR	EGNSSQNWQR	FYQLTKLLDS	
	u87953	Marmoset		VPKDGLKSQE	LFDEIRMTYI	KELGKAIVKR	EGNSSQNWQR	FYQLTKLLDS	
	u87952	Ma'z Monkey		VPKDGLKSQE	LFDEIRMTYI	KELGKAIVKR	EGNSSQNWQR	FYQLTKLLDS	
	Human			VPKDGLKSQE	LFDEIRMTYI	KELGKAIVKR	EGNSSQNWQR	FYQLTKLLDS	
	m14053	rat		VPKEGLKSQE	LFDEIRMTYI	KELGKAIVKR	EGNSSQNWQR	FYQLTKLLDS	
	x04435	mouse		VPKEGLKSQE	LFDEIRMTYI	KELGKAIVKR	EGNSSQNWQR	FYQLTKLLDS	,
	•		675	5 · .				•	

## FIGURE 6 (Continu d)

u87951 Squirrel	MHEVVENLLN	YCFQTFLDKT	MSIEFPEMLA	EIITNQLPKY	SNGNIKKLLF.
AF141371 Pig	MHDVVENLLN	YCFQT		• • • • • • • • • • • • • • • • • • • •	·
113196 Guinea Pig	LHEIVGNLLN	ICFKTFLDKT	MNIEFPEMLA	EIITNQLPKY	SNGDIKKLLF
u87953 Marmoset	MHĘVVENLLN	YCFQTFLDKT	MSIEFPEMLA	EIITNQLPKY	SNGNIRKLLF
u87952 Ma'z Monkey	MHEVVENLLN	YCFQTFLDKT	MSIEFPEMLA	EIITNQLPKY	SNGNIKKLLF
Human	MHEVVENLLN	YCFQTFLDKT	MSIEFPEMLA	EIITNQIPKY	SNGNIKKLLF
m14053 rat	MHEVVENLLT	YCFQTFLDKT	MSIEFPEMLA	EIITNQIPKY	SNGNIKKLLF
x04435 mouse	MHDVVENLLS	YCFQTFLDKS	MSIEFPEMLA	EIITNQIPKY	SNGNIKKLLF
		: .			·
		• • •	•	· · · · · · · · · · · · · · · · · · ·	u
u87951 Squirrel	HQK	· -			
AF141371 Pig	•				
113196 Guinea Pig	. HQK			•	

HQK

HQK

HQK

HQK

HQK

u87953 Marmoset

m14053 rat

x04435 mouse

Human

u87952 Ma z Monkey

FIGURE 7

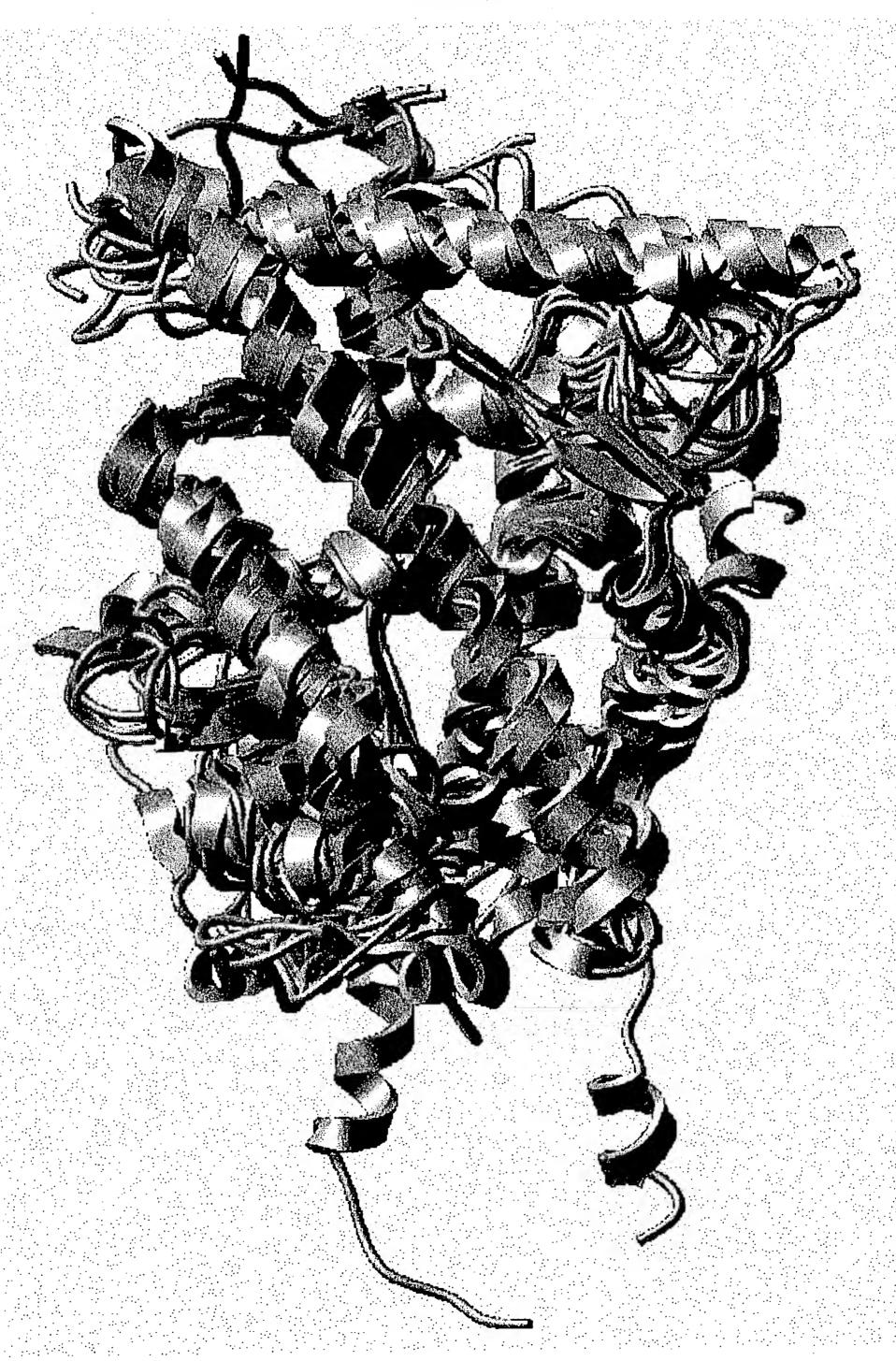


FIGURE 8

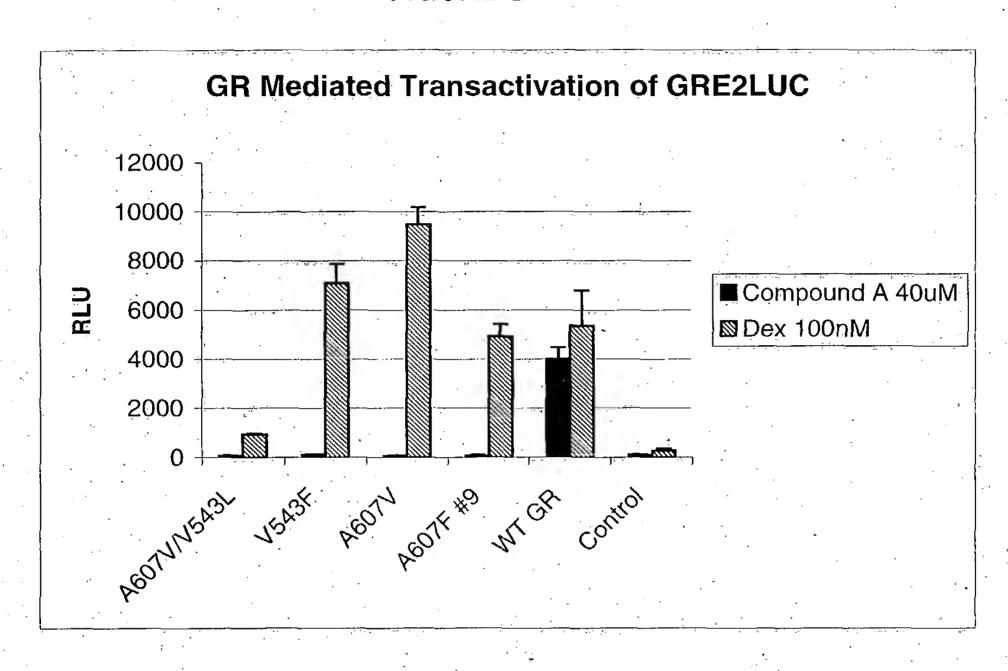
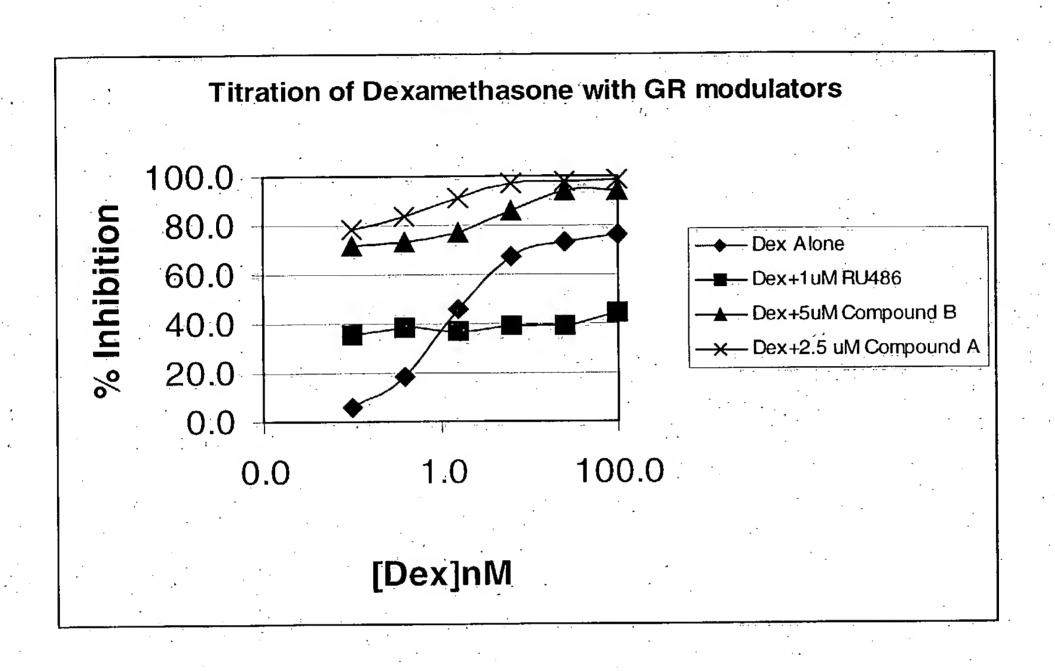


FIGURE 9



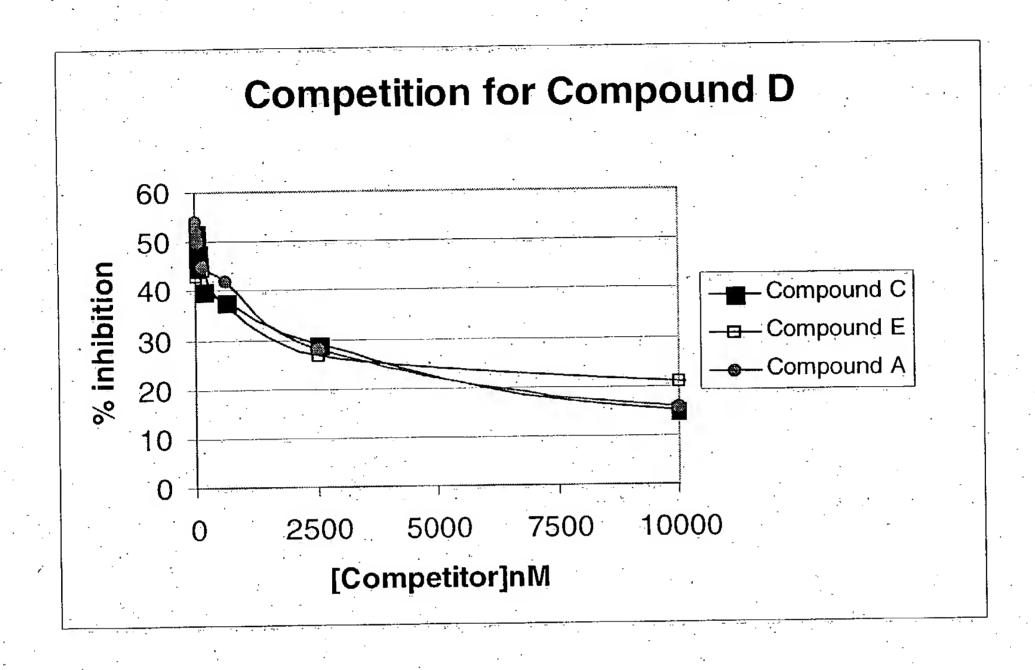


FIGURE 11a

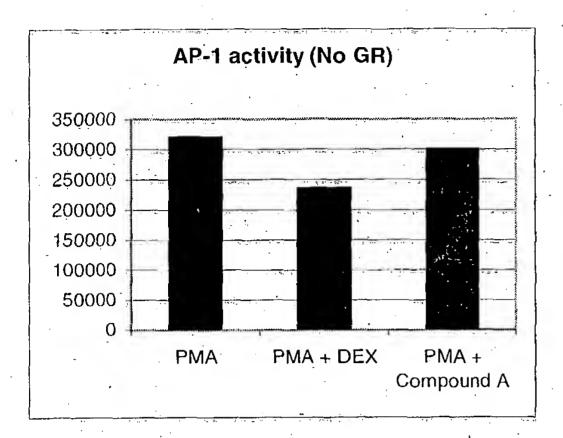


FIGURE 11b

